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KAPELLER-LIBERMANN, ROSANA

<120> 14790, NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR

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<170> PatentIn Ver. 2.1

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Pro Glu Ser Tyr Pro Gln Arg Gln Asp His Glu Leu Gln Ala Leu Glu
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gcc atc tac ggc gcg gac ttc caa gac ctg cgg ccg gac gct tgc gga 203
Ala Ile Tyr Gly Ala Asp Phe Gln Asp Leu Arg Pro Asp Ala Cys Gly
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Pro Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala
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100 105 110

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Tyr His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys
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tct ttt cat gaa gaa atg ctg gaa agg cgg gct cag gag gag cag cag   539
Ser Phe His Glu Glu Met Leu Glu Arg Arg Ala Gln Glu Glu Gln Gln
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agg ctg ttg gag gcc aag cgg aaa gaa gag cag gag caa cgt gaa atc   587
Arg Leu Leu Glu Ala Lys Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile
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ctg cat gag att cag aga agg aaa gaa gag ata aaa gaa gag aaa aaa   635
Leu His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys
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agg aaa gaa atg gct aag cag gaa cgt ttg gaa att gct agt ttg tca   683
Arg Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Ala Ser Leu Ser
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aac caa gat cat acc tct aag aag gac cca gga gga cac aga acg gct   731
Asn Gln Asp His Thr Ser Lys Lys Asp Pro Gly Gly His Arg Thr Ala
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gcc att cta cat gga ggc tct cct gac ttt gta gga aat ggt aaa cat   779
Ala Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys His
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Arg Ala Asn Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val
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tgt aat agt gaa gat tct cct ggc tct tgt gaa att ctg tat ttc aat   875
Cys Asn Ser Glu Asp Ser Pro Gly Ser Cys Glu Ile Leu Tyr Phe Asn
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atg ggg agt cct gat cag ctc atg gtg cac aaa ggg aaa tgt att ggc   923
Met Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Lys Cys Ile Gly
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agt gat gaa caa ctt gga aaa tta gtc tac aat gct ttg gaa aca gcc   971
Ser Asp Glu Gln Leu Gly Lys Leu Val Tyr Asn Ala Leu Glu Thr Ala
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Thr Gly Gly Phe Val Leu Leu Tyr Glu Trp Val Leu Gln Trp Gln Lys
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aaa ttg agc cat cca aat gta gta cgc tac ctt gca atg aat ctc aaa   1163
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            355                 360                 365

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ggg gtc tct ctt gct gca cac ctg agc cac tca ggc ccc atc cct gtg   1259
Gly Val Ser Leu Ala Ala His Leu Ser His Ser Gly Pro Ile Pro Val
    385                 390                 395

cat cag ctt cgc agg tac aca gct cag ctc ctg tca ggc ctt gat tat   1307
His Gln Leu Arg Arg Tyr Thr Ala Gln Leu Leu Ser Gly Leu Asp Tyr
400                 405                 410                 415

ctg cac agc aat tct gtg gtg cat aag gtc ctg agt gca tct aat gtc   1355
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                420                 425                 430

ttg gtg gat gca gaa ggc acc gtc aag att acg gac tat agc att tct   1403
Leu Val Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser
            435                 440                 445

aag cgc ctc gca gac att tgc aag gag gat gtg ttt gag caa acc cga   1451
Lys Arg Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Thr Arg
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Val Arg Phe Ser Asp Asn Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly
    465                 470                 475

gat gtt tgg cgt ctt ggc ctt ctg ctg ctg tcc ctc agc caa gga cag   1547
Asp Val Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln
480                 485                 490                 495

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Glu Cys Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp
                500                 505                 510

ttt caa gat ttt cta aag aaa tgt gtg tgc ttg gat gac aag gaa aga   1643
Phe Gln Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg
            515                 520                 525

tgg agt ccc cag cag ttg ttg aaa cac agc ttt ata aat ccc cag cca   1691
Trp Ser Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro
        530                 535                 540

aaa atg cct cta gtg gaa caa agt cct gaa gat tct gga gga caa gat   1739
Lys Met Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp
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tat gtt gag act gtt att cct agc aac cgg cta ccc agt gct gcc ttc   1787
Tyr Val Glu Thr Val Ile Pro Ser Asn Arg Leu Pro Ser Ala Ala Phe
560                 565                 570                 575

ttt agt gag aca cag aga cag ttt tcc cga tac ttc att gag ttt gaa   1835
Phe Ser Glu Thr Gln Arg Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu
                580                 585                 590

gaa tta caa ctt ctt ggt aaa gga gct ttt gga gct gtc atc aag gtg   1883
Glu Leu Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val
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cag aac aag ttg gac ggc tgc tgc tac gca gtg aag cgc atc ccc atc   1931
Gln Asn Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile
        610                 615                 620

aac ccg gcc agc cgg cag ttc cgc agg atc aag ggc gaa gtg aca ctg   1979
Asn Pro Ala Ser Arg Gln Phe Arg Arg Ile Lys Gly Glu Val Thr Leu
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ctg tca cgg ctg cac cat gag aac att gtg cgc tac tac aac gcc tgg   2027
Leu Ser Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp
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atc gag cgg cac gag cgg ccg gcg gga ccg ggg acg ccg ccc ccg gac   2075
Ile Glu Arg His Glu Arg Pro Ala Gly Pro Gly Thr Pro Pro Pro Asp
                660                 665                 670

tcc ggg ccc ctg gcc aag gat gac cga gct gca cgc ggg cag ccg gcg   2123
Ser Gly Pro Leu Ala Lys Asp Asp Arg Ala Ala Arg Gly Gln Pro Ala
            675                 680                 685

agc gac aca gac ggc ctg gac agc gta gag gcc gcc gcg ccg cca ccc   2171
Ser Asp Thr Asp Gly Leu Asp Ser Val Glu Ala Ala Ala Pro Pro Pro
        690                 695                 700

atc ctc agc agc tcg gtg gag tgg agc act tcg ggc gag cgc tcg gcc   2219
Ile Leu Ser Ser Ser Val Glu Trp Ser Thr Ser Gly Glu Arg Ser Ala
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agt gcc cgt ttc ccc gcc acc ggc ccg ggc tcc agc gat gac gag gac   2267
Ser Ala Arg Phe Pro Ala Thr Gly Pro Gly Ser Ser Asp Asp Glu Asp
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gac gac gag gac gag cac ggt ggc gtc ttc tcc cag tcc ttc ctg cct   2315
Asp Asp Glu Asp Glu His Gly Gly Val Phe Ser Gln Ser Phe Leu Pro
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gct tca gat tct gaa agt gat att atc ttt gac aat gaa gat gag aac   2363
Ala Ser Asp Ser Glu Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn
            755                 760                 765

agt aaa agt cag aat cag gat gaa gat tgc aat gaa aag aat ggc tgc   2411
Ser Lys Ser Gln Asn Gln Asp Glu Asp Cys Asn Glu Lys Asn Gly Cys
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cat gaa agt gag cca tca gtg acg act gag gct gtg cac tac cta tac   2459
His Glu Ser Glu Pro Ser Val Thr Thr Glu Ala Val His Tyr Leu Tyr
    785                 790                 795

atc cag atg gag tac tgt gag aag agc act tta cga gac acc att gac   2507
Ile Gln Met Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp
800                 805                 810                 815

cag gga ctg tat cga gac acc gtc aga ctc tgg agg ctt ttt cga gag   2555
Gln Gly Leu Tyr Arg Asp Thr Val Arg Leu Trp Arg Leu Phe Arg Glu
                820                 825                 830

att ctg gat gga tta gct tat atc cat gag aaa gga atg att cac cgg   2603
Ile Leu Asp Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg
            835                 840                 845

gat ttg aag cct gtc aac att ttt ttg gat tct gat gac cat gtg aaa   2651
Asp Leu Lys Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys
        850                 855                 860

ata ggt gat ttt ggt ttg gcg aca gac cat cta gcc ttt tct gct gac   2699
Ile Gly Asp Phe Gly Leu Ala Thr Asp His Leu Ala Phe Ser Ala Asp
    865                 870                 875

agc aaa caa gac gat cag aca gga gac ttg att aag tca gac cct tca   2747
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880                 885                 890                 895

ggt cac tta act ggg atg gtt ggc act gct ctc tat gta agc cca gag   2795
Gly His Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu
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gtc caa gga agc acc aaa tct gca tac aac cag aaa gtg gat ctc ttc   2843
Val Gln Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe
            915                 920                 925

agc ctg gga att atc ttc ttt gag atg tcc tat cac ccc atg gtc acg   2891
Ser Leu Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr
        930                 935                 940

gct tca gaa agg atc ttt gtt ctc aac caa ctc aga gat ccc act tcg   2939
Ala Ser Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser
    945                 950                 955

cct aag ttt cca gaa gac ttt gac gat gga gag cat gca aag cag aaa   2987
Pro Lys Phe Pro Glu Asp Phe Asp Asp Gly Glu His Ala Lys Gln Lys
960                 965                 970                 975

tca gtc atc tcc tgg ctg ttg aac cac gat cca gca aaa cgg ccc aca   3035
Ser Val Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr
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gcc aca gaa ctg ctc aag agt gag ctg ctg ccc cca ccc cag atg gag   3083
Ala Thr Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu
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Glu Ser Glu Leu His Glu Val Leu His His Thr Leu Thr Asn Val Asp
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ggg aag gcc tac cgc acc atg atg gcc cag atc ttc tcg cag cgc atc   3179
Gly Lys Ala Tyr Arg Thr Met Met Ala Gln Ile Phe Ser Gln Arg Ile
   1025                1030                1035

tcc cct gcc atc gat tac acc tat gac agc gac ata ctg aag ggc aac   3227
Ser Pro Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn
1040                1045                1050                1055

ttc tca atc cgt aca gcc aag atg cag cag cat gtg tgt gaa acc atc   3275
Phe Ser Ile Arg Thr Ala Lys Met Gln Gln His Val Cys Glu Thr Ile
               1060                1065                1070

atc cgc atc ttt aaa aga cat gga gct gtt cag ttg tgt act cca cta   3323
Ile Arg Ile Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu
           1075                1080                1085

ctg ctt ccc cga aac aga caa ata tat gag cac aac gaa gct gcc cta   3371
Leu Leu Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu
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ttc atg gac cac agc ggg atg ctg gtg atg ctt cct ttt gac ctg cgg   3419
Phe Met Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg
   1105                1110                1115

atc cct ttt gca aga tat gtg gca aga aat aat ata ttg aat tta aaa   3467
Ile Pro Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys
1120                1125                1130                1135

cga tac tgc ata gaa cgt gtg ttc agg ccg cgc aag tta gat cga ttt   3515
Arg Tyr Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe
               1140                1145                1150

cat ccc aaa gaa ctt ctg gag tgt gca ttt gat att gtc act tct acc   3563
His Pro Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr
           1155                1160                1165

acc aac agc ttt ctg ccc act gct gaa att atc tac act atc tat gaa   3611
Thr Asn Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu
       1170                1175                1180

atc atc caa gag ttt cca gca ctt cag gaa aga aat tac agt att tat   3659
Ile Ile Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr
   1185                1190                1195

ttg aac cat acc atg tta ttg aaa gca ata ctc tta cac tgt ggg atc   3707
Leu Asn His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys Gly Ile
1200                1205                1210                1215

cca gaa gat aaa ctc agt caa gtc tac att att ctg tat gat gct gtg   3755
Pro Glu Asp Lys Leu Ser Gln Val Tyr Ile Ile Leu Tyr Asp Ala Val
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Thr Glu Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys Asn Leu
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tct ttg tct tct aat agt ctg tgt cga ctc tac aag ttt att gaa cag   3851
Ser Leu Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln
       1250                1255                1260

aag gga gat ttg caa gat ctt atg cca aca ata aat tca tta ata aaa   3899
Lys Gly Asp Leu Gln Asp Leu Met Pro Thr Ile Asn Ser Leu Ile Lys
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cag aaa aca ggt att gca cag ttg gtg aag tat ggc tta aaa gac cta   3947
Gln Lys Thr Gly Ile Ala Gln Leu Val Lys Tyr Gly Leu Lys Asp Leu
1280                1285                1290                1295

gag gag gtt gtt gga ctg ttg aag aaa ctc ggc atc aag tta cag gtc   3995
Glu Glu Val Val Gly Leu Leu Lys Lys Leu Gly Ile Lys Leu Gln Val
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ttg atc aat ttg ggc ttg gtt tac aag gtg cag cag cac aat gga atc   4043
Leu Ile Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Asn Gly Ile
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atc ttc cag ttt gtg gct ttc atc aaa cga agg caa agg gct gta cct   4091
Ile Phe Gln Phe Val Ala Phe Ile Lys Arg Arg Gln Arg Ala Val Pro
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gaa atc ctc gca gct gga ggc aga tat gac ctg ctg att ccc cag ttt   4139
Glu Ile Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro Gln Phe
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aga ggg cca caa gct ctg ggg cca gtt ccc act gcc att ggg gtc agc   4187
Arg Gly Pro Gln Ala Leu Gly Pro Val Pro Thr Ala Ile Gly Val Ser
1360                1365                1370                1375

ata gct ata gac aag ata tct gct gct gtc ctc aac atg gag gaa tct   4235
Ile Ala Ile Asp Lys Ile Ser Ala Ala Val Leu Asn Met Glu Glu Ser
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gtt aca ata agc tct tgt gac ctc ctg gtt gta agt gtt ggt cag atg   4283
Val Thr Ile Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met
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tct atg tcc agg gcc atc aac cta acc cag aaa ctc tgg aca gca ggc   4331
Ser Met Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly
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atc aca gca gaa atc atg tac gac tgg tca cag tcc caa gag gaa tta   4379
Ile Thr Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu
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caa gag tac tgc aga cat cat gaa atc acc tat gtg gcc ctt gtc tcg   4427
Gln Glu Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu Val Ser
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Asp Lys Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys Glu Arg
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cag aca gag aag cgt gtg ctg gag act gaa ctt gtg gac cat gta ctg   4523
Gln Thr Glu Lys Arg Val Leu Glu Thr Glu Leu Val Asp His Val Leu
           1475                1480                1485

cag aaa ctg agg act aaa gtc act gat gaa agg aat ggc aga gaa gct   4571
Gln Lys Leu Arg Thr Lys Val Thr Asp Glu Arg Asn Gly Arg Glu Ala
       1490                1495                1500

tcc gat aat ctt gca gtg caa aat ctg aag ggg tca ttt tct aat gct   4619
Ser Asp Asn Leu Ala Val Gln Asn Leu Lys Gly Ser Phe Ser Asn Ala
   1505                1510                1515

tca ggt ttg ttt gaa atc cat gga gca aca gtg gtt ccc att gtg agt   4667
Ser Gly Leu Phe Glu Ile His Gly Ala Thr Val Val Pro Ile Val Ser
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gtg cta gcc ccg gag aag ctg tca gcc agc act agg agg cgc tat gaa   4715
Val Leu Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg Tyr Glu
               1540                1545                1550

act cag gta caa act cga ctt cag acc tcc ctt gcc aac tta cat cag   4763
Thr Gln Val Gln Thr Arg Leu Gln Thr Ser Leu Ala Asn Leu His Gln
           1555                1560                1565

aaa agc agt gaa att gaa att ctg gct gtg gat cta ccc aaa gaa aca   4811
Lys Ser Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys Glu Thr
       1570                1575                1580

ata tta cag ttt tta tca tta gag tgg gat gct gat gaa cag gca ttt   4859
Ile Leu Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe
   1585                1590                1595

aac aca act gtg aag cag ctg ctg tca cgc ctg cca aag caa aga tac   4907
Asn Thr Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr
1600                1605                1610                1615

ctc aaa tta gtc tgt gat gaa att tat aac atc aaa gta gaa aaa aag   4955
Leu Lys Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys
               1620                1625                1630

gtg tct gtg cta ttt ctg tac agc tat aga gat gac tactacagaa        5001
Val Ser Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp
           1635                1640

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Ile Tyr Gly Ala Asp Phe Gln Asp Leu Arg Pro Asp Ala Cys Gly Pro
         35                  40                  45

Val Lys Glu Pro Pro Glu Ile Asn Leu Val Leu Tyr Pro Gln Gly Leu
     50                  55                  60

Thr Gly Glu Glu Val Tyr Val Lys Val Asp Leu Arg Val Lys Cys Pro
 65                  70                  75                  80

Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala Lys
                 85                  90                  95

Gly Leu Ser Asn Glu Ser Val Asn Leu Leu Lys Ser Arg Leu Glu Glu
            100                 105                 110

Leu Ala Lys Lys His Cys Gly Glu Val Met Ile Phe Glu Leu Ala Tyr
        115                 120                 125

His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys Ser
    130                 135                 140

Phe His Glu Glu Met Leu Glu Arg Arg Ala Gln Glu Glu Gln Gln Arg
145                 150                 155                 160

Leu Leu Glu Ala Lys Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile Leu
                165                 170                 175

His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys Arg
            180                 185                 190

Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Ala Ser Leu Ser Asn
        195                 200                 205

Gln Asp His Thr Ser Lys Lys Asp Pro Gly Gly His Arg Thr Ala Ala
    210                 215                 220
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Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys His Arg
225 230 235 240

Ala Asn Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val Cys
245 250 255

Asn Ser Glu Asp Ser Pro Gly Ser Cys Glu Ile Leu Tyr Phe Asn Met
260 265 270

Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Lys Cys Ile Gly Ser
275 280 285

Asp Glu Gln Leu Gly Lys Leu Val Tyr Asn Ala Leu Glu Thr Ala Thr
290 295 300

Gly Gly Phe Val Leu Leu Tyr Glu Trp Val Leu Gln Trp Gln Lys Lys
305 310 315 320

Met Gly Pro Phe Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys Cys
325 330 335

Lys Lys Gln Ile Gln Gly Thr Glu Thr Glu Phe Asn Ser Leu Val Lys
340 345 350

Leu Ser His Pro Asn Val Val Arg Tyr Leu Ala Met Asn Leu Lys Glu
355 360 365

Gln Asp Asp Ser Ile Val Val Asp Ile Leu Val Glu His Ile Ser Gly
370 375 380

Val Ser Leu Ala Ala His Leu Ser His Ser Gly Pro Ile Pro Val His
385 390 395 400

Gln Leu Arg Arg Tyr Thr Ala Gln Leu Leu Ser Gly Leu Asp Tyr Leu
405 410 415

His Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Asn Val Leu
420 425 430

Val Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser Lys
435 440 445

Arg Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Thr Arg Val
450 455 460

Arg Phe Ser Asp Asn Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly Asp
465 470 475 480

Val Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln Glu
485 490 495

Cys Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp Phe
500 505 510

Gln Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg Trp
515 520 525

Ser Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro Lys
530 535 540

Met Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp Tyr
545 550 555 560

Val Glu Thr Val Ile Pro Ser Asn Arg Leu Pro Ser Ala Ala Phe Phe
565 570 575

Ser Glu Thr Gln Arg Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu Glu
580 585 590

Leu Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val Gln
595 600 605

Asn Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile Asn
610 615 620

Pro Ala Ser Arg Gln Phe Arg Arg Ile Lys Gly Glu Val Thr Leu Leu
625 630 635 640

Ser Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp Ile
645 650 655

Glu Arg His Glu Arg Pro Ala Gly Pro Gly Thr Pro Pro Pro Asp Ser
660 665 670

Gly Pro Leu Ala Lys Asp Asp Arg Ala Ala Arg Gly Gln Pro Ala Ser
675 680 685

Asp Thr Asp Gly Leu Asp Ser Val Glu Ala Ala Ala Pro Pro Pro Ile
690 695 700

Leu Ser Ser Ser Val Glu Trp Ser Thr Ser Gly Glu Arg Ser Ala Ser
705 710 715 720

Ala Arg Phe Pro Ala Thr Gly Pro Gly Ser Ser Asp Asp Glu Asp Asp
725 730 735

Asp Glu Asp Glu His Gly Gly Val Phe Ser Gln Ser Phe Leu Pro Ala
740 745 750

Ser Asp Ser Glu Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn Ser
755 760 765

Lys Ser Gln Asn Gln Asp Glu Asp Cys Asn Glu Lys Asn Gly Cys His
770 775 780

Glu Ser Glu Pro Ser Val Thr Thr Glu Ala Val His Tyr Leu Tyr Ile
785 790 795 800

Gln Met Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp Gln
805 810 815

Gly Leu Tyr Arg Asp Thr Val Arg Leu Trp Arg Leu Phe Arg Glu Ile
820 825 830

Leu Asp Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg Asp
835 840 845

Leu Lys Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys Ile
850 855 860

Gly Asp Phe Gly Leu Ala Thr Asp His Leu Ala Phe Ser Ala Asp Ser
865 870 875 880

Lys Gln Asp Asp Gln Thr Gly Asp Leu Ile Lys Ser Asp Pro Ser Gly
885 890 895

His Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu Val
900 905 910

Gln Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe Ser
915 920 925

Leu Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr Ala
930 935 940

Ser Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser Pro
945 950 955 960

Lys Phe Pro Glu Asp Phe Asp Asp Gly Glu His Ala Lys Gln Lys Ser
965 970 975

Val Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr Ala
980 985 990

Thr Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu Glu
995 1000 1005

Ser Glu Leu His Glu Val Leu His His Thr Leu Thr Asn Val Asp Gly
1010 1015 1020

Lys Ala Tyr Arg Thr Met Met Ala Gln Ile Phe Ser Gln Arg Ile Ser
1025 1030 1035 1040

Pro Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn Phe
1045 1050 1055

Ser Ile Arg Thr Ala Lys Met Gln Gln His Val Cys Glu Thr Ile Ile
1060 1065 1070

Arg Ile Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu Leu
1075 1080 1085

Leu Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu Phe
1090 1095 1100

Met Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg Ile
1105 1110 1115 1120

Pro Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys Arg
1125 1130 1135

Tyr Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe His
1140 1145 1150

Pro Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr Thr
1155 1160 1165

Asn Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu Ile
1170 1175 1180

Ile Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr Leu
1185 1190 1195 1200

Asn His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys Gly Ile Pro
1205 1210 1215

Glu Asp Lys Leu Ser Gln Val Tyr Ile Ile Leu Tyr Asp Ala Val Thr
1220 1225 1230

Glu Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys Asn Leu Ser
1235 1240 1245

Leu Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln Lys
1250 1255 1260

Gly Asp Leu Gln Asp Leu Met Pro Thr Ile Asn Ser Leu Ile Lys Gln
1265 1270 1275 1280

Lys Thr Gly Ile Ala Gln Leu Val Lys Tyr Gly Leu Lys Asp Leu Glu
1285 1290 1295

Glu Val Val Gly Leu Leu Lys Lys Leu Gly Ile Lys Leu Gln Val Leu
1300 1305 1310

Ile Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Asn Gly Ile Ile
1315 1320 1325

Phe Gln Phe Val Ala Phe Ile Lys Arg Arg Gln Arg Ala Val Pro Glu
1330 1335 1340

Ile Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro Gln Phe Arg
1345 1350 1355 1360

Gly Pro Gln Ala Leu Gly Pro Val Pro Thr Ala Ile Gly Val Ser Ile
1365 1370 1375

Ala Ile Asp Lys Ile Ser Ala Ala Val Leu Asn Met Glu Glu Ser Val
1380 1385 1390

Thr Ile Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met Ser
1395 1400 1405

Met Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly Ile
1410 1415 1420

Thr Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu Gln
1425 1430 1435 1440

Glu Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu Val Ser Asp
1445 1450 1455

Lys Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys Glu Arg Gln
1460 1465 1470

Thr Glu Lys Arg Val Leu Glu Thr Glu Leu Val Asp His Val Leu Gln
1475 1480 1485

Lys Leu Arg Thr Lys Val Thr Asp Glu Arg Asn Gly Arg Glu Ala Ser
1490 1495 1500

Asp Asn Leu Ala Val Gln Asn Leu Lys Gly Ser Phe Ser Asn Ala Ser
1505 1510 1515 1520

Gly Leu Phe Glu Ile His Gly Ala Thr Val Val Pro Ile Val Ser Val
1525 1530 1535

Leu Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg Tyr Glu Thr
1540 1545 1550

Gln Val Gln Thr Arg Leu Gln Thr Ser Leu Ala Asn Leu His Gln Lys
1555 1560 1565

Ser Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys Glu Thr Ile
1570 1575 1580

Leu Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn
1585 1590 1595 1600

Thr Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu
1605 1610 1615

Lys Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys Val
1620 1625 1630

Ser Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp
1635 1640

<210> 3
<211> 548
<212> PRT
<213> Homo sapiens

<400> 3
Ala Leu Phe Met Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp
1 5 10 15

Leu Arg Ile Pro Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Ile
20 25 30

Leu Lys Arg Tyr Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp
35 40 45

Arg Phe His Pro Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr
50 55 60

```
Ser Thr Thr Asn Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile
 65                  70                  75                  80

Tyr Glu Ile Ile Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser
                85                  90                  95

Ile Tyr Leu Asn His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys
            100                 105                 110

Gly Ile Pro Glu Asp Lys Leu Ser Gln Val Tyr Ile Ile Leu Tyr Asp
        115                 120                 125

Ala Val Thr Glu Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys
    130                 135                 140

Asn Leu Ser Leu Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile
145                 150                 155                 160

Glu Gln Lys Gly Asp Leu Gln Asp Leu Met Pro Thr Ile Asn Ser Leu
                165                 170                 175

Ile Lys Gln Lys Thr Gly Ile Ala Gln Leu Val Lys Tyr Gly Leu Lys
            180                 185                 190

Asp Leu Glu Glu Val Val Gly Leu Leu Lys Lys Leu Gly Ile Lys Leu
        195                 200                 205

Gln Val Leu Ile Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Asn
    210                 215                 220

Gly Ile Ile Phe Gln Phe Val Ala Phe Ile Lys Arg Arg Gln Arg Ala
225                 230                 235                 240

Val Pro Glu Ile Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro
                245                 250                 255

Gln Phe Arg Gly Pro Gln Ala Leu Gly Pro Val Pro Thr Ala Ile Gly
            260                 265                 270

Val Ser Ile Ala Ile Asp Lys Ile Ser Ala Ala Val Leu Asn Met Glu
        275                 280                 285

Glu Ser Val Thr Ile Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly
    290                 295                 300

Gln Met Ser Met Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr
305                 310                 315                 320

Ala Gly Ile Thr Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu
                325                 330                 335

Glu Leu Gln Glu Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu
            340                 345                 350

Val Ser Asp Lys Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys
        355                 360                 365
```

Glu Arg Gln Thr Glu Lys Arg Val Leu Glu Thr Glu Leu Val Asp His
370 375 380

Val Leu Gln Lys Leu Arg Thr Lys Val Thr Asp Glu Arg Asn Gly Arg
385 390 395 400

Glu Ala Ser Asp Asn Leu Ala Val Gln Asn Leu Lys Gly Ser Phe Ser
405 410 415

Asn Ala Ser Gly Leu Phe Glu Ile His Gly Ala Thr Val Val Pro Ile
420 425 430

Val Ser Val Leu Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg
435 440 445

Tyr Glu Thr Gln Val Gln Thr Arg Leu Gln Thr Ser Leu Ala Asn Leu
450 455 460

His Gln Lys Ser Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys
465 470 475 480

Glu Thr Ile Leu Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln
485 490 495

Ala Phe Asn Thr Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln
500 505 510

Arg Tyr Leu Lys Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu
515 520 525

Lys Lys Val Ser Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp Tyr Tyr
530 535 540

Arg Ile Leu Phe
545

<210> 4
<211> 1648
<212> PRT
<213> Murine Species

<400> 4
Met Ala Gly Gly Arg Gly Ala Ser Gly Arg Gly Arg Ala Glu Pro Gln
1 5 10 15

Glu Ser Tyr Ser Gln Arg Gln Asp His Glu Leu Gln Ala Leu Glu Ala
20 25 30

Ile Tyr Gly Ser Asp Phe Gln Asp Leu Arg Pro Asp Ala Arg Gly Arg
35 40 45

Val Arg Glu Pro Pro Glu Ile Asn Leu Val Leu Tyr Pro Gln Gly Leu
50 55 60

Ala Gly Glu Glu Val Tyr Val Gln Val Glu Leu Gln Val Lys Cys Pro
65 70 75 80

```
Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala Lys
                85                  90                  95

Gly Leu Ser Asn Glu Ser Val Asn Leu Leu Lys Ser His Leu Glu Glu
            100                 105                 110

Leu Ala Lys Lys Gln Cys Gly Glu Val Met Ile Phe Glu Leu Ala His
        115                 120                 125

His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys Ser
    130                 135                 140

Phe His Glu Glu Met Leu Glu Arg Gln Ala Gln Glu Lys Gln Gln Arg
145                 150                 155                 160

Leu Leu Glu Ala Arg Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile Leu
                165                 170                 175

His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys Arg
            180                 185                 190

Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Thr Ser Leu Thr Asn
        195                 200                 205

Gln Asp Tyr Ala Ser Lys Arg Asp Pro Ala Gly His Arg Ala Ala Ala
    210                 215                 220

Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys Ala Arg
225                 230                 235                 240

Thr Tyr Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val Cys
                245                 250                 255

Ser Gly Glu Pro Ser Pro Gly Ser Cys Asp Ile Leu His Phe Ser Val
            260                 265                 270

Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Arg Cys Val Gly Ser
        275                 280                 285

Asp Glu Gln Leu Gly Lys Val Val Tyr Asn Ala Leu Glu Thr Ala Thr
    290                 295                 300

Gly Ser Phe Val Leu Leu His Glu Trp Val Leu Gln Trp Gln Lys Met
305                 310                 315                 320

Gly Pro Cys Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys Cys Lys
                325                 330                 335

Arg Gln Ile Gln Gly Ala Glu Thr Glu Phe Ser Ser Leu Val Lys Leu
            340                 345                 350

Ser His Pro Asn Ile Val Arg Tyr Phe Ala Met Asn Ser Arg Glu Glu
        355                 360                 365

Glu Asp Ser Ile Val Ile Asp Ile Leu Ala Glu His Val Ser Gly Ile
    370                 375                 380
```

Ser Leu Ala Thr His Leu Ser His Ser Gly Pro Val Pro Ala His Gln
385 390 395 400

Leu Arg Lys Tyr Thr Ala Gln Leu Leu Ala Gly Leu Asp Tyr Leu His
405 410 415

Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Ser Val Leu Val
420 425 430

Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser Lys Arg
435 440 445

Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Ala Arg Val Arg
450 455 460

Phe Ser Asp Ser Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly Asp Val
465 470 475 480

Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln Glu Cys
485 490 495

Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp Phe Gln
500 505 510

Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg Trp Ser
515 520 525

Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro Lys Leu
530 535 540

Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp Tyr Ile
545 550 555 560

Glu Thr Val Ile Pro Ser Asn Gln Leu Pro Ser Ala Ala Phe Phe Ser
565 570 575

Glu Thr Gln Lys Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu Glu Leu
580 585 590

Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val Gln Asn
595 600 605

Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile Asn Pro
610 615 620

Ala Ser Arg His Phe Arg Arg Ile Lys Gly Glu Val Thr Leu Leu Ser
625 630 635 640

Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp Ile Glu
645 650 655

Arg His Glu Arg Pro Ala Val Pro Gly Thr Pro Pro Pro Asp Cys Thr
660 665 670

Pro Gln Ala Gln Asp Ser Pro Ala Thr Cys Gly Lys Thr Ser Gly Asp
675 680 685

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Thr Glu Glu Leu Gly Ser Val Glu Ala Ala Ala Pro Pro Pro Ile Leu
    690                 695                 700

Ser Ser Ser Val Glu Trp Ser Thr Ser Ala Glu Arg Ser Thr Ser Thr
705                 710                 715                 720

Arg Phe Pro Val Thr Gly Gln Asp Ser Ser Ser Asp Glu Glu Asp Glu
                725                 730                 735

Asp Glu Arg Asp Gly Val Phe Ser Gln Ser Phe Leu Pro Ala Ser Asp
            740                 745                 750

Ser Asp Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn Ser Lys Ser
        755                 760                 765

Gln Asn Gln Asp Glu Asp Cys Asn Gln Lys Asp Gly Ser His Glu Ile
    770                 775                 780

Glu Pro Ser Val Thr Ala Glu Ala Val His Tyr Leu Tyr Ile Gln Met
785                 790                 795                 800

Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp Gln Gly Leu
                805                 810                 815

Phe Arg Asp Thr Ser Arg Leu Trp Arg Leu Phe Arg Glu Ile Leu Asp
            820                 825                 830

Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg Asp Leu Lys
        835                 840                 845

Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys Ile Gly Asp
    850                 855                 860

Phe Gly Leu Ala Thr Asp His Leu Ala Phe Thr Ala Glu Gly Lys Gln
865                 870                 875                 880

Asp Asp Gln Ala Gly Asp Gly Val Ile Lys Ser Asp Pro Ser Gly His
                885                 890                 895

Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu Val Gln
            900                 905                 910

Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe Ser Leu
        915                 920                 925

Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr Ala Ser
    930                 935                 940

Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser Pro Lys
945                 950                 955                 960

Phe Pro Asp Asp Phe Asp Asp Gly Glu His Thr Lys Gln Lys Ser Val
                965                 970                 975

Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr Ala Met
            980                 985                 990
```

Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu Glu Ser
995 1000 1005

Glu Leu His Glu Val Leu His His Thr Leu Ala Asn Ile Asp Gly Lys
1010 1015 1020

Ala Tyr Arg Thr Met Met Ser Gln Ile Phe Cys Gln His Ile Ser Pro
1025 1030 1035 1040

Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn Phe Leu
1045 1050 1055

Ile Arg Thr Ala Lys Ile Gln Gln Leu Val Cys Glu Thr Ile Val Arg
1060 1065 1070

Val Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu Leu Leu
1075 1080 1085

Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu Phe Met
1090 1095 1100

Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg Val Pro
1105 1110 1115 1120

Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys Arg Tyr
1125 1130 1135

Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe His Pro
1140 1145 1150

Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr Thr Asn
1155 1160 1165

Ser Ser Leu Pro Thr Ala Glu Thr Ile Tyr Thr Ile Tyr Glu Ile Ile
1170 1175 1180

Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr Leu Asn
1185 1190 1195 1200

His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys Gly Ile Pro Glu
1205 1210 1215

Asp Lys Leu Ser Gln Val Tyr Val Ile Leu Tyr Asp Ala Val Thr Glu
1220 1225 1230

Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys Asn Leu Ser Leu
1235 1240 1245

Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln Lys Gly
1250 1255 1260

Asp Leu Gln Asp Leu Thr Pro Thr Ile Asn Ser Leu Ile Lys Gln Lys
1265 1270 1275 1280

Thr Gly Val Ala Gln Leu Val Lys Tyr Ser Leu Lys Asp Leu Glu Asp
1285 1290 1295

```
Val Val Gly Leu Leu Lys Lys Leu Gly Val Lys Leu Gln Val Ser Ile
          1300                1305                1310

Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Thr Gly Ile Ile Phe
       1315                1320                1325

Gln Phe Leu Ala Phe Ser Lys Arg Arg Gln Arg Val Val Pro Glu Ile
   1330                1335                1340

Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro Lys Phe Arg Gly
1345                1350                1355                1360

Pro Gln Thr Val Gly Pro Val Pro Thr Ala Val Gly Val Ser Ile Ala
               1365                1370                1375

Ile Asp Lys Ile Phe Ala Val Val Leu Asn Met Glu Glu Pro Val Thr
          1380                1385                1390

Val Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met Ser Met
       1395                1400                1405

Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly Ile Thr
   1410                1415                1420

Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu Gln Glu
1425                1430                1435                1440

Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu Val Ser Asp Lys
               1445                1450                1455

Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys Glu Arg Gln Thr
          1460                1465                1470

Glu Lys Arg Val Leu Glu Ser Asp Leu Val Asp His Val Met Gln Lys
       1475                1480                1485

Leu Arg Thr Lys Val Gly Asp Glu Arg Asn Phe Arg Asp Ala Ser Asp
   1490                1495                1500

Asn Leu Ala Val Gln Thr Leu Lys Gly Ser Phe Ser Asn Ala Ser Gly
1505                1510                1515                1520

Leu Phe Glu Ile His Gly Thr Thr Val Val Pro Asn Val Ile Val Leu
               1525                1530                1535

Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg His Glu Ile Gln
          1540                1545                1550

Val Gln Thr Arg Leu Gln Thr Thr Leu Ala Asn Leu His Gln Lys Ser
       1555                1560                1565

Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys Glu Thr Ile Leu
   1570                1575                1580

Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn Thr
1585                1590                1595                1600
```

Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu Lys
1605 1610 1615

Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys Val Ser
1620 1625 1630

Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile Leu Phe
1635 1640 1645

<210> 5
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<220>
<223> each "Xaa" represents a variable amino acid

<220>
<223> this peptide may encompass a deletion peptide consisting of 10-19 residues at positions 31-49

<400> 5
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly Xaa Xaa Xaa Xaa
1 5 10 15

Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Arg Asp
115 120 125

Xaa Lys Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Asp Phe Gly Xaa Xaa Xaa Xaa
145 150 155 160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165 170 175

Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp
180 185 190

Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
210 215 220

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225 230 235 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Xaa
245 250 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa
260 265 270

<210> 6
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<220>
<223> each "Xaa" represents a variable amino acid

<220>
<223> this peptide may encompass a deletion peptide consisting of 15-23 residues at positions 7-29

<400> 6
Gly Xaa Gly Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys
20 25 30

<210> 7
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 7
Ile Leu Lys Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys
1 5 10 15

```
Arg Leu Ser His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp
            20                  25                  30

Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Gly Asp
        35                  40                  45

Leu Phe Asp Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala
    50                  55                  60

Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser
65                  70                  75                  80

Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
                85                  90                  95

Glu Asn Gly Thr Val Lys Ile Ala Asp
            100                 105
```

<210> 8
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 8

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Arg Leu Pro Leu Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu
  1               5                  10                  15

Lys Lys Cys Leu Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr
            20                  25                  30

Ala Lys Glu Ile Leu Asn His Pro Trp Phe
        35                  40
```

<210> 9
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 9

```
Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
  1               5                  10                  15

Lys Ala Lys His Lys Thr Gly Lys Ile Val Ala Val Lys Ile Leu Lys
            20                  25                  30

Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys Arg Leu Ser
        35                  40                  45
```

```
His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp Thr Asp Asp
     50                  55                  60

His Leu
 65
```

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<210> 10
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      kinase sequence

<400> 10
His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Gly Asp Leu Phe Asp
  1               5                  10                  15

Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala Lys Lys Ile
             20                  25                  30

Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser Asn Gly Ile
         35                  40                  45

Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Asn Gly
     50                  55                  60

Thr Val Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Leu Glu Lys Leu
 65                  70                  75                  80

Thr Thr Phe Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile
                 85                  90                  95

Leu Glu Gly Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly
            100                 105                 110

Val Ile Leu Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala
        115                 120                 125

Asp Leu Pro Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile
    130                 135                 140

Phe Val Leu Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile
145                 150                 155                 160

Asp Pro Leu Glu Glu Leu Phe Arg Ile Lys Lys Arg Arg Leu Pro Leu
                165                 170                 175

Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu
            180                 185                 190

Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile
        195                 200                 205
```

Leu Asn His Pro Trp Phe
210

<210> 11
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 11
Thr Asp Ile Ile Lys Tyr Pro Val Ile Thr Glu Lys Leu Ala Met Asn
1 5 10 15

Leu Leu Glu Glu Pro Asn Lys
20

<210> 12
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 12
Asn Gln Thr Thr Glu Arg Val Tyr Glu Leu His Lys Ile Glu Leu Phe
1 5 10 15

Ser Val Pro Glu Leu Asn Gly Lys Lys Ile Gly Leu Gly Ile Lys Leu
20 25 30

Pro Lys Thr Asp Thr Glu Ser Leu Arg Thr Met Val Ala Lys Leu Leu
35 40 45

Gly Leu Ala Met Lys Thr Lys Thr Phe Pro Asp Asp Glu Gly Ser Gln
50 55 60

Pro Val Ser Phe Glu Arg Lys Asp Leu Glu Glu Ser Leu Lys Glu Lys
65 70 75 80

Asp Tyr Phe Val Cys Glu Lys Thr Asp Gly Ile Arg Cys Ser His Gly
85 90 95

Phe Asn Arg Thr Gly Phe Leu Ile Ala Ala Leu Leu Phe Leu Val Glu
100 105 110

His Pro Gly Leu Glu Glu Ala Ile Ser His Ile Leu Ser Gly Glu Phe
115 120 125

Leu Ile Asp Arg Glu Lys Asn Tyr Tyr Lys Gln Asp Tyr Ile Asp Leu
130 135 140

Leu Pro Lys Arg Leu Phe Pro Arg Glu Lys Asp Lys Thr Lys Ala Lys
145 150 155 160

Glu Leu Pro Thr Tyr His Arg Gly Thr Leu Leu Asp Gly Glu Leu Val
165 170 175

Ile Asp Ile Asn Arg Ile Ala Val Glu Gln Lys Thr Leu Arg Tyr Val
180 185 190

Val Phe Asp Ala Leu Ala Ile Ser Gly Gln Thr Val Ile Gln Arg Asp
195 200 205

Leu Ser Lys Arg Leu Gly Asp Glu Phe Ile Lys Ala Val Lys Lys Pro
210 215 220

Phe Asp Glu Phe Lys Lys Val Met Pro Asp Ala Lys Ile Leu Asn Gln
225 230 235 240

Gln Lys Tyr Asn Phe Pro Phe Lys Ile Gly Leu Lys His Met Ser Leu
245 250 255

Ser Tyr Gly Gln Leu Lys Leu Leu Lys Ala Glu Ser Lys Met Val Ile
260 265 270

Ser Lys Ala Asp Ala Met Pro Lys Leu Leu His Ile Asn Asp Gly Leu
275 280 285

Ile Phe Thr Cys Val Arg Asp Thr Pro Tyr Ile Glu Gly Glu Ile Leu
290 295 300

Val Glu Pro Gly Asn Ser Tyr Leu Asp Phe Asn Leu Leu Lys Trp Lys
305 310 315 320

Pro Lys Glu Glu Asn Thr Val Asp Phe Glu Leu Ile Leu Glu Phe Glu
325 330 335

Glu Val Asn Asp Pro Glu Leu Asp Glu Lys Asp Gly Phe Ser Leu Tyr
340 345 350

Leu Asp Tyr Asp Ala Met Pro Gly Glu Leu Phe Lys Phe Ser Leu Gly
355 360 365

Val Trp Gln Gly Gly Phe Asn Lys Arg Phe Glu Val Ile His Thr Asp
370 375 380

Gln Ile Phe Phe Arg Val Ala Phe Gln Lys Leu Gly Arg Leu Lys His
385 390 395 400

Glu Phe Ala Glu Leu Ser Val Ser Asp Lys Asp Trp Tyr Lys Leu Lys
405 410 415

Ala Leu Glu Gln Pro Leu Asp Gly Arg Ile Val Glu Cys Arg Leu Ala
420 425 430

Asp Ile Glu Ile Leu Ile Phe Gln Glu Gly Arg Trp Glu Tyr Leu Arg
435 440 445

Phe Arg Asp Asp Lys Gln Gln Ala Leu Lys Thr Gly Gly Tyr Ser Gly
450 455 460

Asn His Ile Ser Thr Val Glu Lys Val Leu Leu Ser Ile Lys Asp Gly
465 470 475 480

Val Ser Ile Glu Glu Leu Leu Lys Leu Phe Pro Gly Met Tyr Phe Ala
485 490 495

Gly Ala Lys Thr Leu Ile Lys Arg
500

<210> 13
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 13
Tyr Glu Leu Leu Lys Lys Leu Gly Lys Gly Ala Phe Gly Lys Val Tyr
1 5 10 15

Leu Ala Arg Asp Lys Lys Thr Gly Arg Leu Val Ala Ile Lys Val Ile
20 25 30

Lys Glu Arg Ile Leu Arg Glu Ile Lys Ile Leu Lys Lys Asp His Pro
35 40 45

Asn Ile Val Lys Leu Tyr Asp Val Phe Glu Asp Asp Lys Leu Tyr Leu
50 55 60

Val Met Glu Tyr Cys Glu Gly Asp Leu Gly Asp Leu Phe Asp Leu Leu
65 70 75 80

Lys Lys Arg Gly Arg Arg Gly Leu Arg Lys Val Leu Ser Glu Glu Ala
85 90 95

Arg Phe Tyr Phe Arg Gln Ile Leu Ser Ala Leu Glu Tyr Leu His Ser
100 105 110

Gln Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
115 120 125

Ser His Val Lys Leu Ala Asp Phe Gly Leu Ala Arg Gln Leu Thr Thr
130 135 140

Phe Val Gly Thr Pro Glu Tyr Met Ala Pro Glu Val Leu Gly Tyr Gly
145 150 155 160

Lys Pro Ala Val Asp Ile Trp Ser Leu Gly Cys Ile Leu Tyr Glu Leu
165 170 175

Leu Thr Gly Lys Pro Pro Phe Pro Gln Leu Asp Leu Ile Phe Lys Lys
180 185 190

Ile Gly Ser Pro Glu Ala Lys Asp Leu Ile Lys Lys Leu Leu Val Lys
195 200 205

Asp Pro Glu Lys Arg Leu Thr Ala Glu Ala Leu Glu Asp Glu Leu Asp
210 215 220

Ile Lys Ala His Pro Phe Phe
225 230

<210> 14
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 14
Tyr Glu Leu Leu Lys Lys Leu Gly Lys Gly Ala Phe Gly Lys Val Tyr
1 5 10 15

Leu Ala Arg Asp Lys Lys Thr Gly Arg Leu Val Ala Ile Lys Val Ile
20 25 30

Lys Glu Arg Ile Leu Arg Glu Ile Lys Ile Leu Lys Lys Asp His Pro
35 40 45

Asn Ile Val Lys Leu Tyr Asp Val Phe Glu Asp Asp Lys Leu Tyr Leu
50 55 60

Val Met Glu Tyr Cys Glu Gly Asp Leu Gly Asp Leu Phe Asp Leu Leu
65 70 75 80

Lys Lys Arg Gly Arg Arg Gly Leu Arg Lys Val Leu Ser Glu Glu Ala
85 90 95

Arg Phe Tyr Phe Arg Gln Ile Leu Ser Ala Leu Glu Tyr Leu His Ser
100 105 110

Gln Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
115 120 125

Ser His Val Lys Leu Ala Asp Phe Gly Leu Ala Arg Gln Leu Thr Thr
130 135 140

Phe Val Gly Thr Pro Glu Tyr Met Ala Pro Glu Val Leu Gly Tyr Gly
145 150 155 160

Lys Pro Ala Val Asp Ile Trp Ser Leu Gly Cys Ile Leu Tyr Glu Leu
165 170 175

Leu Thr Gly Lys Pro Pro Phe Pro Gln Leu Asp Leu Ile Phe Lys Lys
180 185 190

Ile Gly Ser Pro Glu Ala Lys Asp Leu Ile Lys Lys Leu Leu Val Lys
195 200 205

Asp Pro Glu Lys Arg Leu Thr Ala Glu Ala Leu Glu Asp Glu Leu Asp
210 215 220

Ile Lys Ala His Pro Phe Phe
225 230

<210> 15
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 15
Leu Thr Leu Gly Lys Lys Leu Gly Glu Gly Ala Phe Gly Glu Val Tyr
1 5 10 15

Lys Gly Thr Leu Lys Ile Glu Val Ala Val Lys Thr Leu Lys Glu Asp
20 25 30

Ala Lys Glu Glu Phe Leu Arg Glu Ala Lys Ile Met Lys Lys Leu Gly
35 40 45

Gly Lys His Pro Asn Ile Val Lys Leu Leu Gly Val Cys Thr Glu Glu
50 55 60

Gly Arg Arg Phe Met Glu Val Glu Pro Leu Met Ile Val Met Glu Tyr
65 70 75 80

Met Glu Gly Gly Asp Leu Leu Asp Tyr Leu Arg Lys Asn Arg Pro Lys
85 90 95

Leu Ser Leu Ser Asp Leu Leu Ser Phe Ala Leu Gln Ile Ala Lys Gly
100 105 110

Met Glu Tyr Leu Glu Ser Lys Asn Phe Val His Arg Asp Leu Ala Ala
115 120 125

Arg Asn Cys Leu Val Gly Glu Asn Lys Val Val Lys Ile Ser Asp Phe
130 135 140

Gly Leu Ser Arg Asp Leu Tyr Asp Asp Asp Lys Lys Gly Glu Ser Lys
145 150 155 160

Asp Tyr Tyr Arg Lys Lys Gly Gly Lys Gly Gly Lys Thr Leu Leu Pro
165 170 175

Ile Arg Trp Met Ala Pro Glu Ser Leu Lys Asp Gly Lys Phe Thr Ser
180 185 190

Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Thr
195 200 205

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Leu Gly Glu Gln Pro Tyr Pro Gly Glu Ile Gln Gln Phe Met Ser Asn
    210                 215                 220

Glu Glu Val Leu Glu Tyr Leu Lys Lys Gly Tyr Arg Leu Pro Lys Pro
225                 230                 235                 240

Glu Asn Asp Leu Pro Ile Ser Ser Val Thr Cys Pro Asp Glu Leu Tyr
                245                 250                 255

Asp Leu Met Leu Gln Cys Trp Ala Glu Asp Pro Glu Asp Arg Pro Thr
            260                 265                 270

Phe Ser Glu Leu Val Glu Arg Leu
        275                 280


<210> 16
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      kinase sequence

<400> 16
Ser Phe Arg Glu Arg Gln Ala Gln Glu Leu Glu Val Ile Lys Ser Ile
  1               5                  10                  15

Phe Gly Cys Asp Val Glu Asp Leu Arg Pro Gln Ala Asn Pro Ser Leu
             20                  25                  30

Trp Lys Pro Thr Asp Ile Arg Ile Gln Leu Thr Pro Leu Arg Asp Ser
         35                  40                  45

Ser Asn Gly Leu Glu Thr Tyr Val Cys Thr Lys Leu His Val Thr Cys
     50                  55                  60

Pro Ser Lys Tyr Pro Lys Leu Pro Pro Lys Ile Ser Leu Glu Glu Ser
 65                  70                  75                  80

Lys Gly Met Ser Asp Gln Leu Leu Glu Ala Leu Arg Asn Gln Leu Gln
                85                  90                  95

Ala Gln Ser Gln Glu Leu Arg Gly Glu Val Met Ile Tyr Glu Leu Ala
            100                 105                 110

Gln Thr Val Gln Ala Phe Leu Leu Glu His Asn Lys Pro Pro Lys Gly
        115                 120                 125

Ser Phe Tyr Asp Gln Met Leu Gln Asp Lys Gln Lys Arg Asp Gln Glu
    130                 135                 140


<210> 17
<211> 54
<212> PRT
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 17
Glu Thr Leu Tyr Phe His Lys Met Gly Arg Gln Ile Gln Arg Gly Cys
1 5 10 15

Cys Val Gly His Ser Gln Arg Gly Cys Ile Ala Tyr Thr Gly Ile Asp
20 25 30

Met His Cys Gly Gln Leu Leu Tyr Ile Thr Glu Trp Asn Ile Lys Tyr
35 40 45

Ser Gln Leu Glu Gln Pro
50

<210> 18
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 18
Leu Lys Ser Leu Met Arg Gly Lys Gly Glu Ala Ala Ser Leu Ala Arg
1 5 10 15

Gly Ala Leu Arg Glu Leu Glu Thr Val Val Gly Leu Ala Tyr Ser Leu
20 25 30

Gly Val Lys Cys Pro Ile His Ile Trp Ala Gly Leu Pro Ile Ser Phe
35 40 45

Asp Arg Ala Ser Asn Gly Gly Ile Val Trp Gln Met Thr Ala Asp Leu
50 55 60

Lys Pro Asn Arg Ser Gly His Pro Ser Val Leu Ala Ile Gly Glu Arg
65 70 75 80

Tyr Asp Ser Met Leu His Glu Phe Gln Lys Gln Ala Gln Lys Phe Asn
85 90 95

Pro Ala Met Pro Ala Arg Gly Val Leu Ser Gly Ala Gly Leu Thr Phe
100 105 110

Ser Leu Asp Lys Leu Val Ala Ala Val Gly Val Glu Tyr Ala Lys Asp
115 120 125

Cys Arg Ala Ile Asp Val Gly Ile Cys Val Cys Gly Thr Arg Pro Pro
130 135 140

Leu Lys Asp Val Thr Tyr Ile Met Arg Leu Leu Trp Ser Val Gly Ile
145 150 155 160

Arg Cys Gly Ile Val Glu Ala Ala Ser Glu Leu Gly Asp Glu Ala Gln
165 170 175

Asp Leu Ala Arg Leu Gly Ala Leu His Val Ile Leu Val Ala Glu Asn
180 185 190

Gly Ser Leu Arg Val Arg Ser Phe Glu Arg Glu Arg Phe Gln Glu Arg
195 200 205

His Leu Thr Arg Thr Glu Leu Val Glu Phe Ile Gln Lys Met Leu Arg
210 215 220

Ser Asp Gly Leu Asn Gly Thr Thr Val Asp Asn Phe Ser His Leu Ser
225 230 235 240

Ala Leu Gly Ser Gly Asp Asn Arg Ser Ser Gly Gly Lys Glu Arg Glu
245 250 255

Arg Gly Glu Asn Gly Leu Ser Thr Ser Ala Ser Asn Ala Thr Ile Lys
260 265 270

Asn Asn Tyr Ser Gln Leu Pro Asn Leu Gln Val Thr Phe Leu Thr His
275 280 285

Asp Lys Pro Thr Ala Asn Tyr Lys Arg Arg Leu Glu Asn Gln Val Ala
290 295 300

Gln Gln Met Ser Ser Thr Leu Ser Gln Phe Leu Lys Lys Glu Thr Phe
305 310 315 320

Val Val Leu Val Val Glu Leu Pro Pro Ala Val Val
325 330

<210> 19
<211> 296
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 19
Val Leu Ser Gly Ala Gly Leu Thr Phe Ser Leu Asp Lys Leu Val Ala
1 5 10 15

Ala Val Gly Val Glu Tyr Ala Lys Asp Cys Arg Ala Ile Asp Val Gly
20 25 30

Ile Cys Val Cys Gly Thr Arg Pro Pro Leu Lys Asp Val Thr Tyr Ile
35 40 45

Met Arg Leu Leu Trp Ser Val Gly Ile Arg Cys Gly Ile Val Glu Ala
50 55 60

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Ala Ser Glu Leu Gly Asp Glu Ala Gln Asp Leu Ala Arg Leu Gly Ala
 65                  70                  75                  80

Leu His Val Ile Leu Val Ala Glu Asn Gly Ser Leu Arg Val Arg Ser
                85                  90                  95

Phe Glu Arg Glu Arg Phe Gln Glu Arg His Leu Thr Arg Thr Glu Leu
            100                 105                 110

Val Glu Phe Ile Gln Lys Met Leu Arg Ser Asp Gly Leu Asn Gly Thr
        115                 120                 125

Thr Val Asp Asn Phe Ser His Leu Ser Ala Leu Gly Ser Gly Asp Asn
    130                 135                 140

Arg Ser Ser Gly Gly Lys Glu Arg Glu Arg Gly Glu Asn Gly Leu Ser
145                 150                 155                 160

Thr Ser Ala Ser Asn Ala Thr Ile Lys Asn Asn Tyr Ser Gln Leu Pro
                165                 170                 175

Asn Leu Gln Val Thr Phe Leu Thr His Asp Lys Pro Thr Ala Asn Tyr
            180                 185                 190

Lys Arg Arg Leu Glu Asn Gln Val Ala Gln Gln Met Ser Ser Thr Leu
        195                 200                 205

Ser Gln Phe Leu Lys Lys Glu Thr Phe Val Val Leu Val Val Glu Leu
    210                 215                 220

Pro Pro Ala Val Val Asn Ala Ile Val Gly Ala Ile Asn Pro Arg Glu
225                 230                 235                 240

Ile Arg Lys Arg Glu Thr Glu Pro Glu Ile Asn Tyr Val Ile Glu Arg
                245                 250                 255

Phe Ser Lys Tyr Lys Arg Tyr Ile Ser Glu Ile Asn Glu Glu Val Val
            260                 265                 270

Asp Tyr Leu Ser Asp Ala Lys Thr Pro Ile Val Ala Leu Tyr Ser Ile
        275                 280                 285

Ser Asp Ser Tyr Tyr Arg Val Ile
    290                 295
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<210> 20
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 20
Asp Gln Gly Gly Glu Leu Leu Ser Leu Arg Tyr Asp Leu Thr Val Pro
1 5 10 15

Phe Ala Arg Tyr Val Ala Met Asn Leu Leu Lys Val Thr Asn Leu Pro
20 25 30

Leu Lys Arg Tyr His Ile Ala Lys Val Tyr Arg Arg Asp Arg Pro Ala
35 40 45

Met Thr Arg Gly Arg Tyr Arg Glu Phe Tyr Gln Cys Asp Phe Asp Ile
50 55 60

Ile Gly Glu Tyr Asp Thr Met Ala Pro Asp Ala Glu Ile Leu Lys Ile
65 70 75 80

Leu Thr Glu Ile Leu Ser Gln Leu Gly Ile Arg Glu Leu Gly Asn Phe
85 90 95

Lys Ile Lys Ile Asn His Arg Gly Ile Leu Asp Ser Leu Leu Gln Pro
100 105 110

Trp Pro Lys Thr Leu Gln Glu Tyr Leu Thr Gln Tyr Lys Ala
115 120 125

<210> 21
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 21
Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Glu Ser His Glu Asn
1 5 10 15

Thr Pro Asn Met Ile Lys Leu Ile Ala Asp Phe Gly Leu Ala Lys Glu
20 25 30

Ile Tyr Ser Ser Ser Ser Thr Tyr Glu Glu Met Ser Ser Ser Gln Ala
35 40 45

Val Phe Gly Ser His Gln Thr Thr Ser Thr Met Cys Gly Thr Pro Tyr
50 55 60

Tyr Val Ser Met Lys Ser Met Ala Pro Glu Tyr Met Ala Pro Glu Ser
65 70 75 80

Ser Ala Thr Asn Tyr Gln Lys Tyr Ser Thr Lys Ser Asp Val Trp Ser
85 90 95

Phe Gly Val Ile Leu Tyr Glu Met
100

<210> 22
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 22
Gln Leu Met His Tyr Val His Gln Ile Ala Lys Gly Leu Glu Tyr Leu
1 5 10 15

His Ser Lys Asn Gln Lys His Gln Gly Ile Ile His Arg Ala Lys Lys
20 25 30

Val Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Glu Ser His Glu
35 40 45

Asn Thr Pro Asn Met Ile Lys Leu Ile Ala Asp Phe Gly Leu Ala Lys
50 55 60

Glu Ile Tyr Ser Ser Ser Ser Thr Tyr Glu Glu Met Ser Ser Ser Gln
65 70 75 80

Ala Val Phe Gly Ser His Gln Thr Thr Ser Thr Met Cys Gly Thr Pro
85 90 95

Tyr Tyr Val Ser
100

<210> 23
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 23
Glu Gly Ser Leu Val Glu Tyr Met Glu Tyr Met Ser Gly Gly Ser Glu
1 5 10 15

Asp Tyr Met Lys Lys Leu Ser Leu Glu Thr Val Met Lys Ile Ala Met
20 25 30

Met Ile Leu Gln Phe Met Gln Ile Met His Met Ser Ser Glu Ser Glu
35 40 45

Ser Leu Ser His Ser Gln Leu Met His Tyr Val His Gln Ile Ala Lys
50 55 60

Gly Leu Glu Tyr Leu His Ser Lys Asn Gln Lys His Gln Gly Ile Ile
65 70 75 80

His Arg Ala Lys Lys Val Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
85 90 95

Glu Glu Ser His Glu Asn Thr Pro Asn Met Ile Lys Leu Ile Ala Asp
100 105 110

Phe Gly Leu Ala Lys Glu Ile
115

<210> 24
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 24
Tyr Met Ala Pro Glu Ser Ser Ala Thr Asn Tyr Gln Lys Tyr Ser Thr
1 5 10 15

Lys Ser Asp Val Trp Ser Phe Gly Val Ile Leu Tyr Glu Met Leu Thr
20 25 30

Gly Lys Pro Pro Phe Phe Pro Gly Glu Ser Glu Val Ser Glu Glu Glu
35 40 45

Pro Tyr Gln Ser Met Lys Asn Met Glu Val Leu Glu Met Gly Pro Glu
50 55 60

Glu Thr Ile Gln Lys Val Met Ser Lys Ile Val Glu Lys Lys Gly Glu
65 70 75 80

Arg Met Pro Gln Pro Ser Ser Ser Asn Cys Pro Glu Val Ser Gln Glu
85 90 95

Ala Lys Asp Leu Leu Lys Lys Cys Leu Gln Lys Asp Pro Glu Lys Arg
100 105 110

Arg Pro Thr Phe Glu Glu Ile Leu Gln His
115 120

<210> 25
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 25
Gln Tyr Glu Leu Leu Lys Lys Leu Leu Gly Lys Gly Ser Phe Gly Lys
1 5 10 15

Val Tyr Lys Ala Lys His Lys
20

<210> 26
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 26
Glu Val Ser Gln Glu Ala Lys Asp Leu Leu Lys Lys Cys Leu Gln Lys
1 5 10 15

Asp Pro Glu Lys Arg Arg Pro Thr Phe Glu Glu Ile Leu Gln His Pro
20 25 30

Trp Phe Leu Met Arg Asn Pro
35

<210> 27
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 27
Leu Gly Thr Gly Ser Phe Gly Ala Val Tyr Lys
1 5 10

<210> 28
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 28
Leu Asp Gln Asn Gly Thr Val Leu Gln Leu Pro Phe Asp Leu Met Met
1 5 10 15

Gly His Ala Arg Ser Leu Ala Arg Ile Thr Asn Ser Pro Val Val Gln
20 25 30

Lys Ser Tyr Ser Phe Gly Asn Ile Phe Arg Asp Arg His Gly Gly Gly
35 40 45

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 30
Glu Ala Glu Leu Ala Arg Leu Ala Gln Ser Glu Lys Glu Arg Glu Glu
1 5 10 15

Arg Lys Lys Leu Glu Glu Ser Lys Glu Glu Glu Arg Val Leu Glu Asp
20 25 30

Met Leu Gln Glu Glu Leu Lys Arg Gln Arg Asn Lys Ala Lys Glu Ser
35 40 45

<210> 31
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 31
Arg Asn Lys Ala Lys Glu Ser Arg Lys Lys Asn Arg Ser His Gln Leu
1 5 10 15

Ser Pro Asp Arg Ala Pro Gln Asp Pro Gly Glu Thr Asp Glu Thr Leu
20 25 30

Met Phe Asp Gln Pro Cys Lys Ile Thr Asp Gly Ser Gly Asn Ala Leu
35 40 45

Phe Phe Gln Thr Val Ile Gly Lys Thr Val Phe
50 55

<210> 32
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus kinase sequence

<400> 32
Leu Glu Glu Ser Lys Glu Glu Glu Arg Val Leu Glu Asp Met Leu Gln
1 5 10 15

Glu Glu Leu Lys Arg Gln Arg Asn Lys Ala Lys Glu Ser Arg Lys Lys
20 25 30

Asn Arg Ser His Gln Leu Ser Pro Asp Arg Ala Pro Gln Asp Pro Gly
35 40 45

Glu Thr Asp Glu Thr Leu Met Phe Asp Gln Pro Cys Lys Ile Thr Asp
50 55 60

Gly Ser Gly Asn Ala Leu Phe Phe Gln Thr Val Ile Gly Lys Thr Val
65 70 75 80

Phe Arg Glu

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